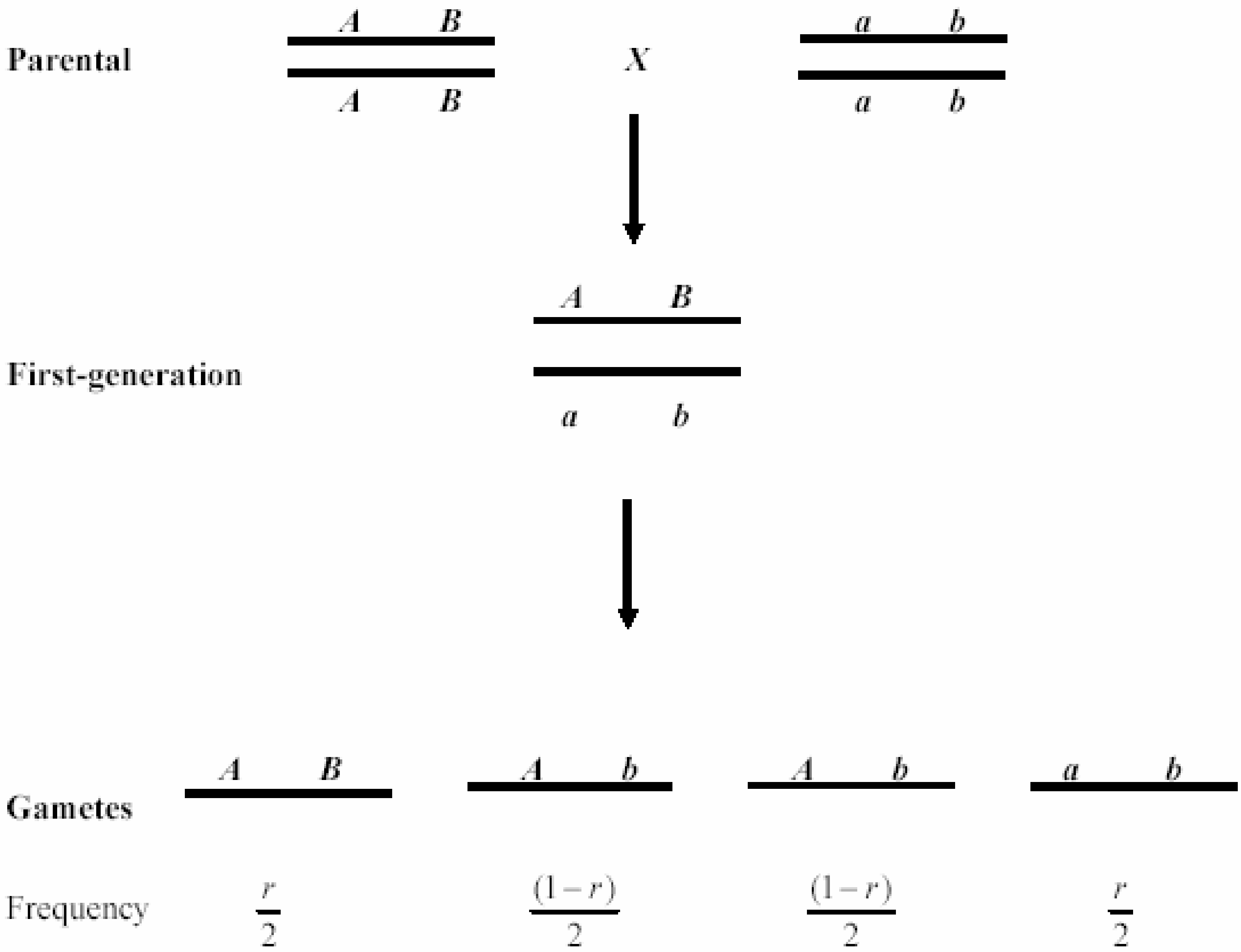
CHAPTER 10

MULTIPLE LOCI

Population geneticists are often accused of having failed to incorporate the findings of modern molecular genetics. But the situation is far worse than that. They have not even incorporated the findings of Morgan. Nearly the entire corpus of literature in theoretical population genetics is written from the standpoint of single Mendelian genes or else genes that all obey the law of independent segregation.

Richard C. Lewontin (1970)

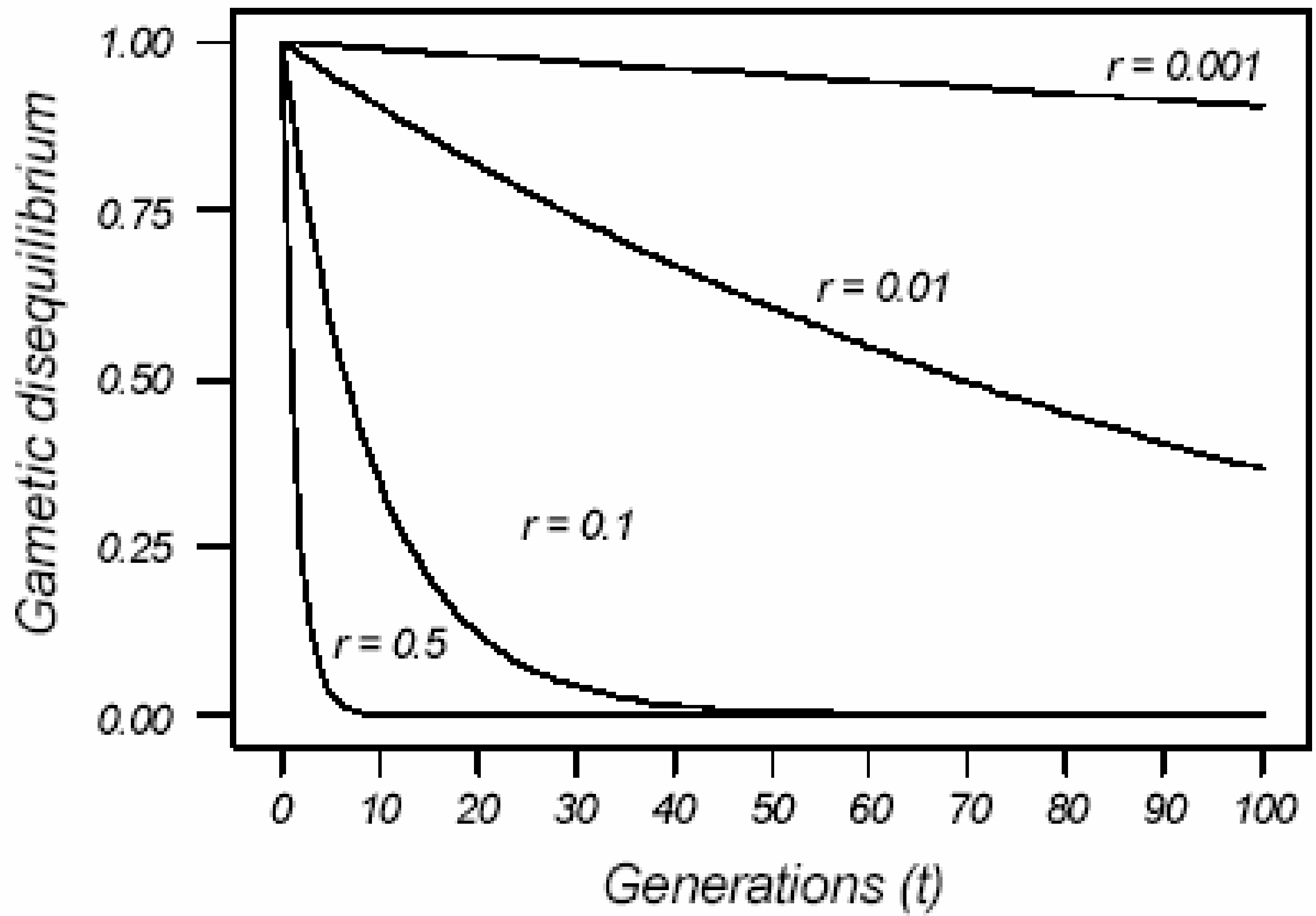

Parental
A B
A B
X
a b
a b
First-generation
A B
a b
Gametes
A B
A b
A b
a b
Frequency
$\frac{r}{2}$
$\frac{(1-r)}{2}$
$\frac{(1-r)}{2}$
$\frac{r}{2}$

Gamete	Frequency
AB	$G_1 = (p_1)\,(p_2)$
Ab	$G_2 = (p_1)\,(q_2)$
aB	$G_3 = (q_1)\,(p_2)$
ab	$G_4 = (q_1)\,(q_2)$

$$D = (G_1 G_4) - (G_2 G_3)$$

Gametic (linkage) disequilibrium

Gamete	$D = 0$	D(max)
$A\ B$	$(p_1)(p_2) = 0.24$	0.40
$a\ B$	$(q_1)(p_2) = 0.16$	0.00
$A\ b$	$(p_1)(q_2) = 0.36$	0.20
$a\ b$	$(q_1)(q_2) = 0.24$	0.40



Gametic disequilibrium
1.00
0.75
0.50
0.25
0.00
r = 0.001
r = 0.01
r = 0.1
r = 0.5
0
10
20
30
40
50
60
70
80
90
100
Generations (t)

	Cutthroat trout (CT)		Rainbow trout (RT)
P	*AABBCC.....ZZ/M*	X	*aabbcc.....zz/m*
	(CT ♀ X RT ♂)	↓	(CT ♂ X RT ♀)
F1	*AaBbCc.....Zz/M*		*AaBbCc.....Zz/m*
		↓	

F2	*AaBBcc....ZZ/M*	*AaBBCc....ZZ/M*	*AaBbcc....ZZ/M*
	AABBcc....ZZ/M	*AaBBCC....ZZ/M*	*AaBBcc....ZZ/M*
	AABBcc....ZZ/M	*aaBBcc....ZZ/M*	*Aabbcc....ZZ/M*
	Many other genotypes		

	Genotype frequencies				
Genotypes	Parental	First gen	Second gen	Third gen	Equilibrium
AABB	0.500	0.250	0.141	0.098	0.063
AABb			0.094	0.118	0.125
AAbb			0.016	0.035	0.063
AaBB			0.094	0.118	0.125
AaBb		0.500	0.312	0.267	0.250
Aabb			0.094	0.118	0.125
aaBB			0.016	0.035	0.063
aaBb			0.094	0.118	0.125
aabb	0.500	0.250	0.141	0.098	0.063
D	---	+0.250	+0.125	+0.063	0.000

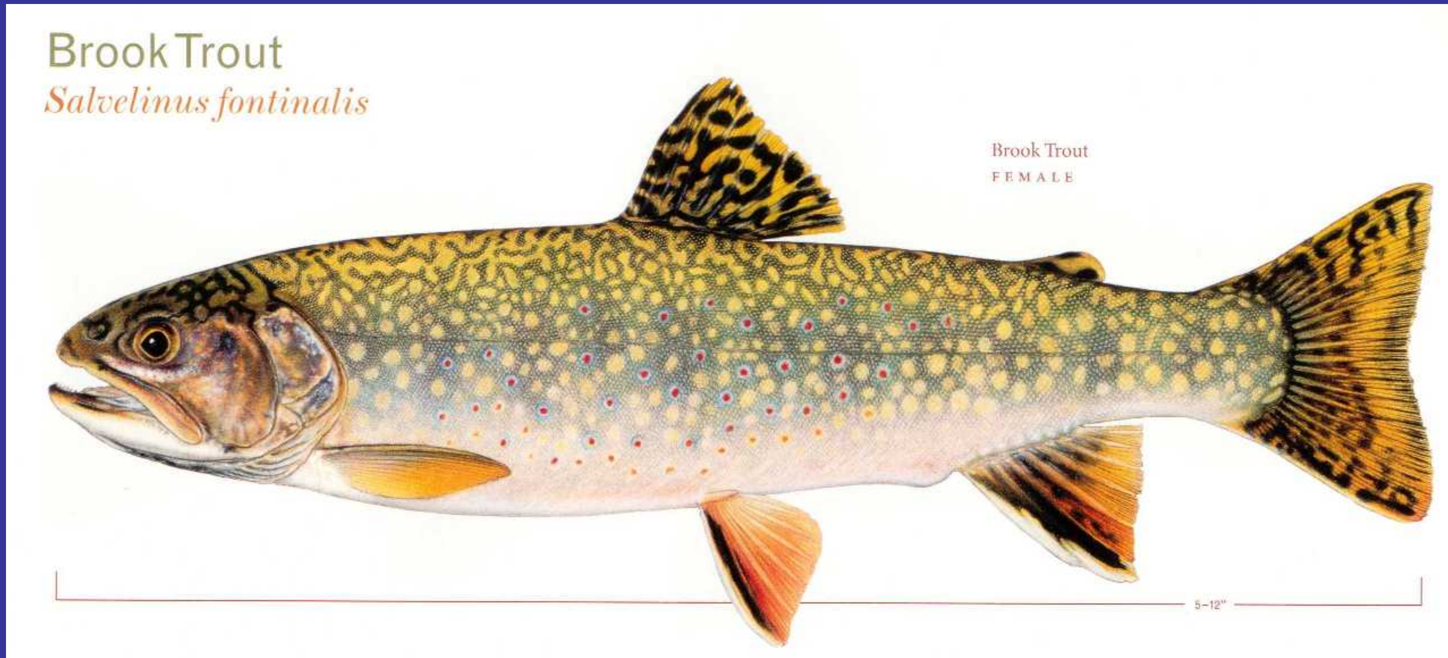

Brook Trout
Salvelinus fontinalis
Brook Trout
FEMALE
5–12"


illustration copyright 2001 Joseph R. Tomelleri

	Bull trout (BT)		Brook trout (ST)
P	AABBCC/M	X	aabbcc/m
F1	AaBbCc/M		AaBbCc/m
	[BT ♀ x ST ♂]		[BT ♂ x ST ♀]

Further Crosses

AABbCC/M	AABbCC/m
AAbbcc/M	AAbbcc/m
aaBbCc/M	aaBbCc/m
many /M	many /m

Allozyme genotypes at 8 nuclear loci and mtDNA genotypes in a sample of bull trout and brook trout in Mission Creek, Montana.

		Nuclear encoded loci								
No.	mtDNA	Aat1	Ck-A1	IDDH	sIDHP-2	LDH-A1	LDH-B2	MDH-A2	sSOD-1	Status
1	L	LR	LR	LR	LR	LR	LR	LR	LR	F1
2	L	LR	LR	LR	LR	LR	LR	LR	LR	F1
3	L	R	R	LR	LR	LR	LR	LR	R	F1xBR
4	L	L	L	L	L	L	L	L	L	BL
5	L	LR	LR	LR	LR	LR	LR	LR	LR	F1
6	R	LR	LR	LR	LR	LR	LR	LR	LR	F1
7	L	LR	LR	LR	LR	LR	LR	LR	LR	F1
8	R	LR	LR	LR	LR	LR	LR	LR	LR	F1
9	R	LR	LR	LR	LR	LR	LR	LR	LR	F1
10	L	LR	LR	LR	LR	LR	LR	LR	LR	F1
11	R	LR	LR	LR	LR	LR	LR	LR	LR	F1
12	R	LR	LR	LR	LR	LR	LR	LR	LR	F1
13	R	R	R	R	R	R	R	R	R	BR
14	R	R	R	R	R	R	R	R	R	BR
15	R	R	R	R	R	R	R	R	R	BR

L= homozygous for bull trout allele; R= homozygous for brook trout allele; LR= heterozygous for bull trout and brook trout alleles.

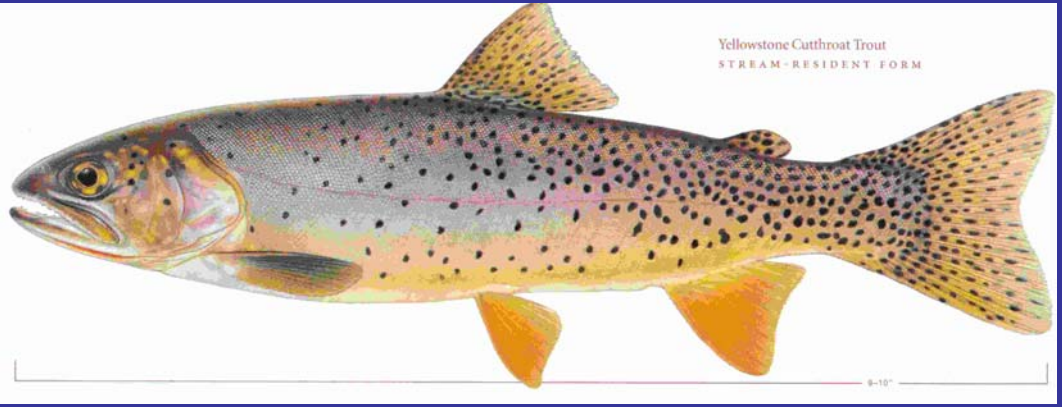
Bull trout = BL (*L* = homozygous)

Brook trout = BR (*R* = homozygous)

Westslope cutthroat trout

(WCT)

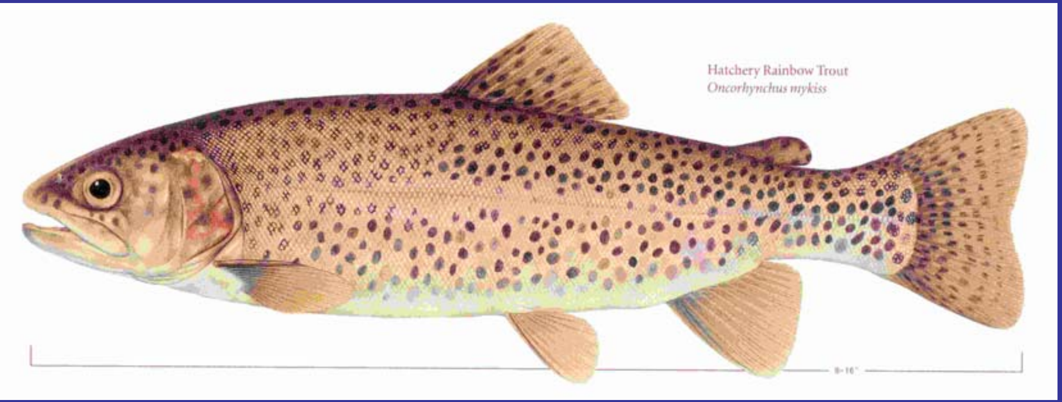
Oncorhynchus clarki lewisi



Yellowstone cutthroat trout

(YCT)

O. c. bouvieri



Rainbow trout

(RT)

O. mykiss

(Illustrations by Joseph R. Tomelleri)

Genotypes at eight diagnostic allozyme loci and mtDNA from Forest Lake, Montana.

		Nuclear encoded loci							
No.	*mtDNA*	*Aat1*	*Gpi3*	*Idh1*	*Lgg*	*Me1*	*Me3*	*Me4*	*Sdh*
1	YS	W	W	WY	W	W	W	W	Y
2	YS	W	WY	WY	WY	Y	W	WY	Y
3	WS	WY	Y	Y	W	Y	WY	Y	WY
4	WS	Y	W	WY	WY	W	Y	W	WY
5	YS	Y	Y	Y	WY	WY	WY	Y	Y
6	YS	WY	Y	W	WY	W	W	W	Y
7	WS	WY	WY	Y	W	WY	W	W	W
8	WS	WY	Y	WY	WY	Y	W	Y	Y
9	WS	Y	Y	WY	WY	W	WY	WY	W
10	WS	WY	Y	WY	WY	WY	Y	W	Y
11	YS	Y	W	W	WY	W	Y	W	Y
12	WS	W	WY	Y	WY	W	WY	WY	Y
13	YS	W	Y	W	Y	W	WY	W	W
14	YS	Y	Y	WY	WY	WY	WY	WY	W
15	WS	WY	Y	WY	Y	W	Y	WY	W

W = *homozygous for westslope allele; Y = homozygous for Yellowstone allele; WY = heterozygous for westslope and Yellowstone alleles.*

W = homozygous WCT

WY = heterozygous

Y = homozygous YCT

No.	mtDNA	*Aat1*	*Gpi3*	*Idb1*
1	YS	W	W	WY
2	YS	W	WY	WY
3	WS	WY	Y	Y
4	WS	Y	W	WY
5	YS	Y	Y	Y
6	YS	WY	Y	W
7	WS	WY	WY	Y
8	WS	WY	Y	WY
9	WS	Y	Y	WY
10	WS	WY	Y	WY
11	YS	Y	W	W
12	WS	W	WY	Y
13	YS	W	Y	W
14	YS	Y	Y	WY
15	WS	WY	Y	WY

W = homozygous for westslope allele; Y = homozygous for Yellowston

Hybrid swarm: a population of individuals that all are hybrids by varying numbers of generations of backcrossing with parental types and mating among hybrids.

Here be sparred owls.

CHAPTER 11

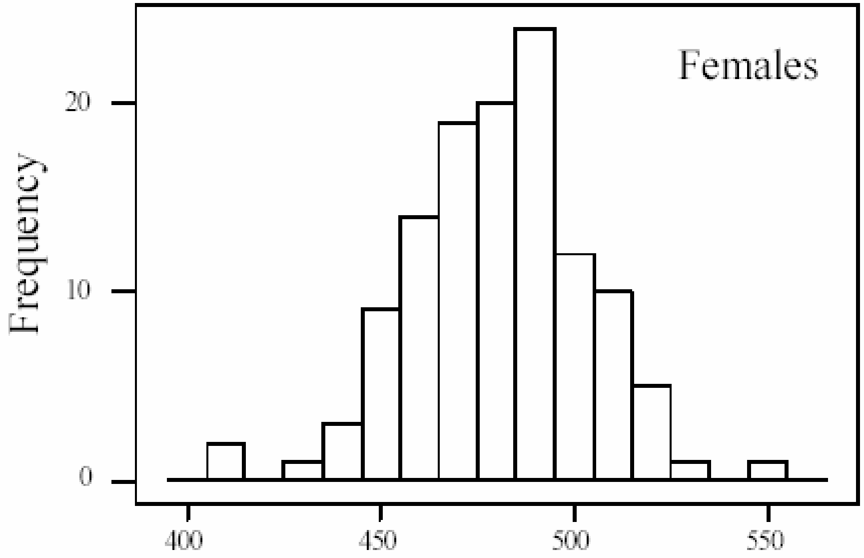
QUANTITATIVE GENETICS

Most of the major genetic concerns in conservation biology, including inbreeding depression, loss of evolutionary potential, genetic adaptation to captivity, and outbreeding depression, involve quantitative genetics.

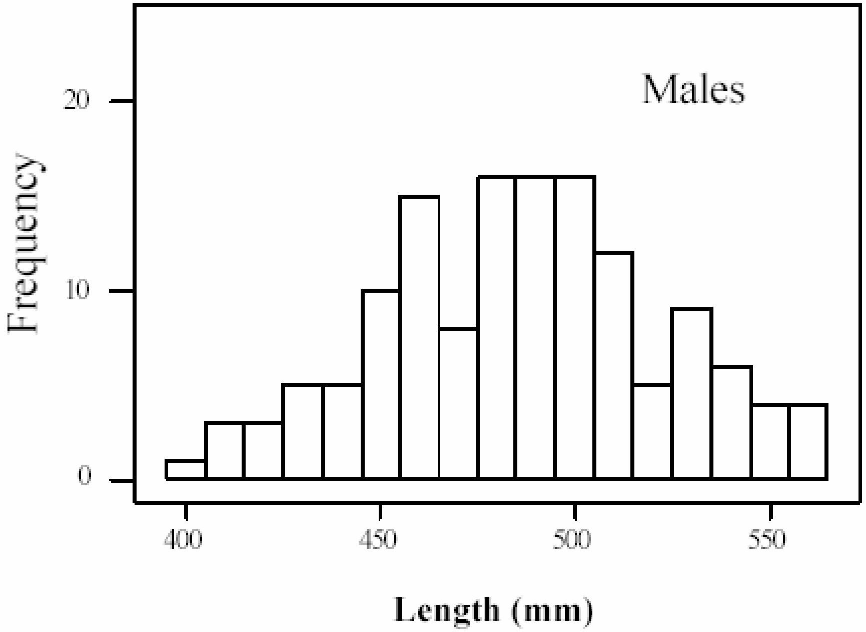
Richard Frankham (1999)

An overview of theoretical and empirical results in quantitative genetics provides some insight into the critical population sizes below which species begin to experience genetic problems that exacerbate the risk of extinction.

Michel Lynch (1996)

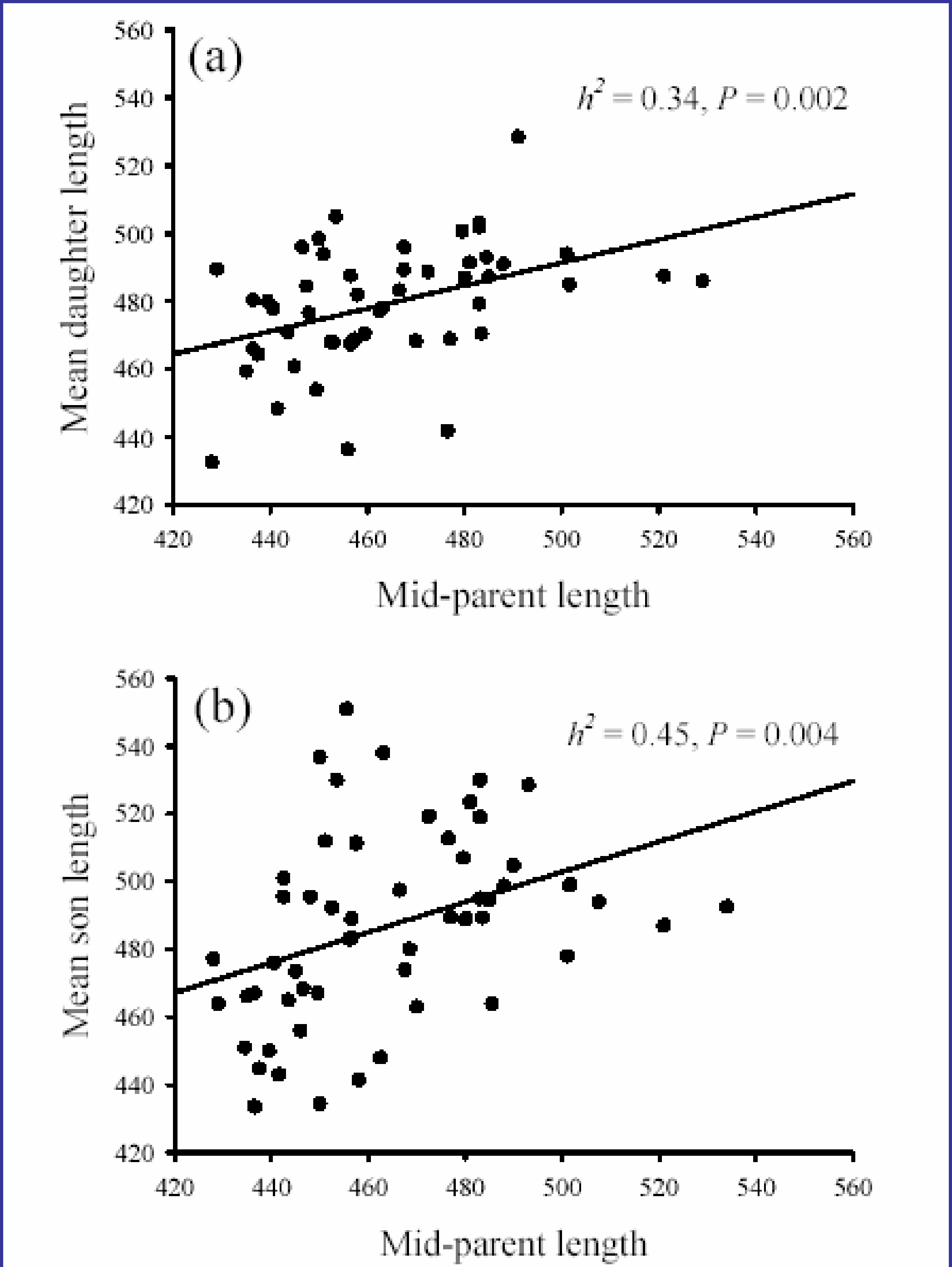

Females
Frequency
20
10
0
400
450
500
550

Pink salmon


Males
Frequency
20
10
0
400
450
500
550
Length (mm)

$$V_P = V_G + V_E$$

$$\text{Heritability} = V_G / V_P$$



(a)
$h^2 = 0.34, P = 0.002$
Mean daughter length
Mid-parent length
(b)
$h^2 = 0.45, P = 0.004$
Mean son length
Mid-parent length

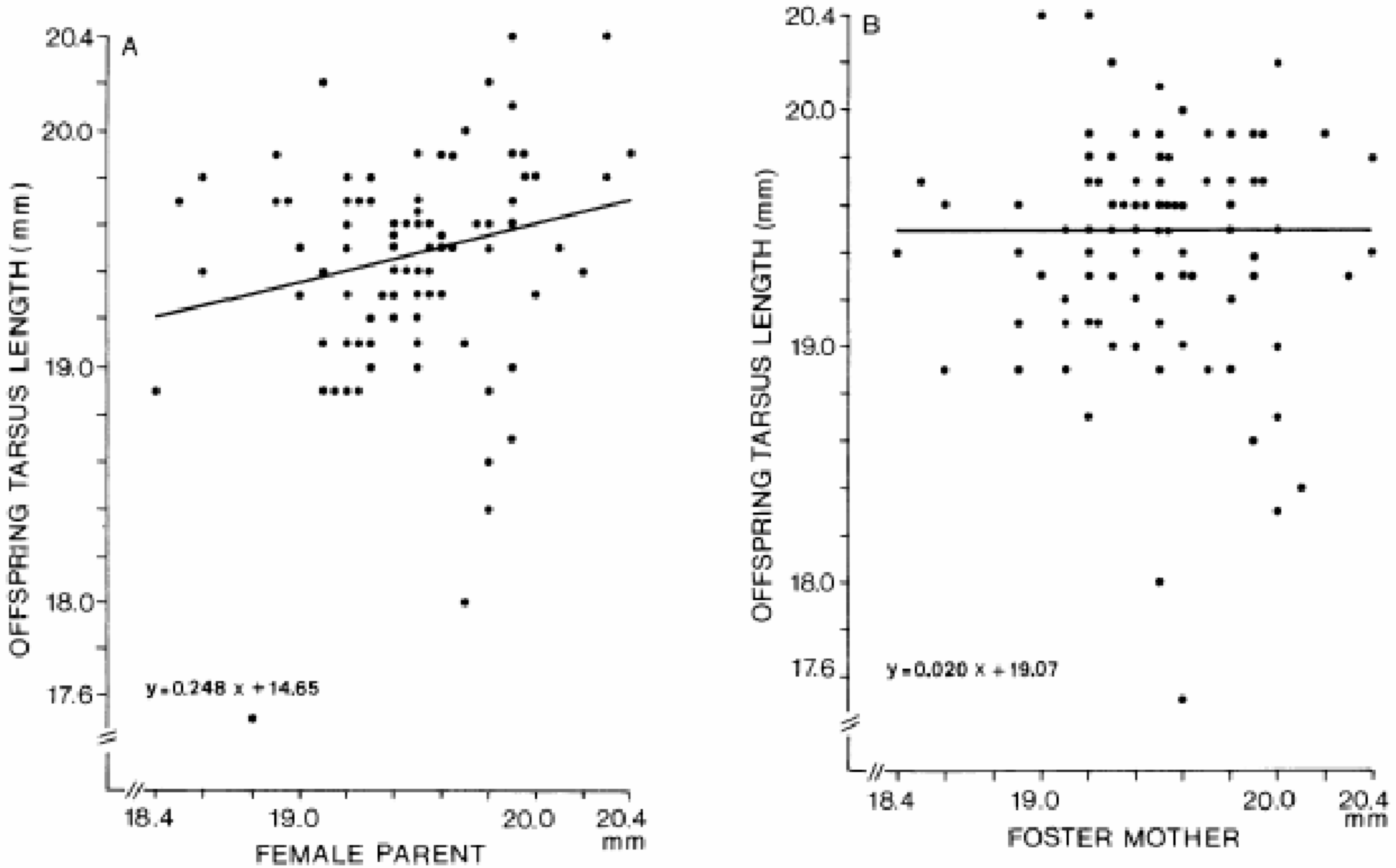


Figure 11.3. Mother-offspring regression estimation of heritability of tarsus length in the pied flycatcher (H_N=0.53; Alatalo and Lundberg 1986). Each point represents the mean tarsus length of progeny from one nest.

We expect heritability to be lost during a bottleneck at the same rate as heterozygosity:

$$\Delta h = -\frac{1}{2N}$$

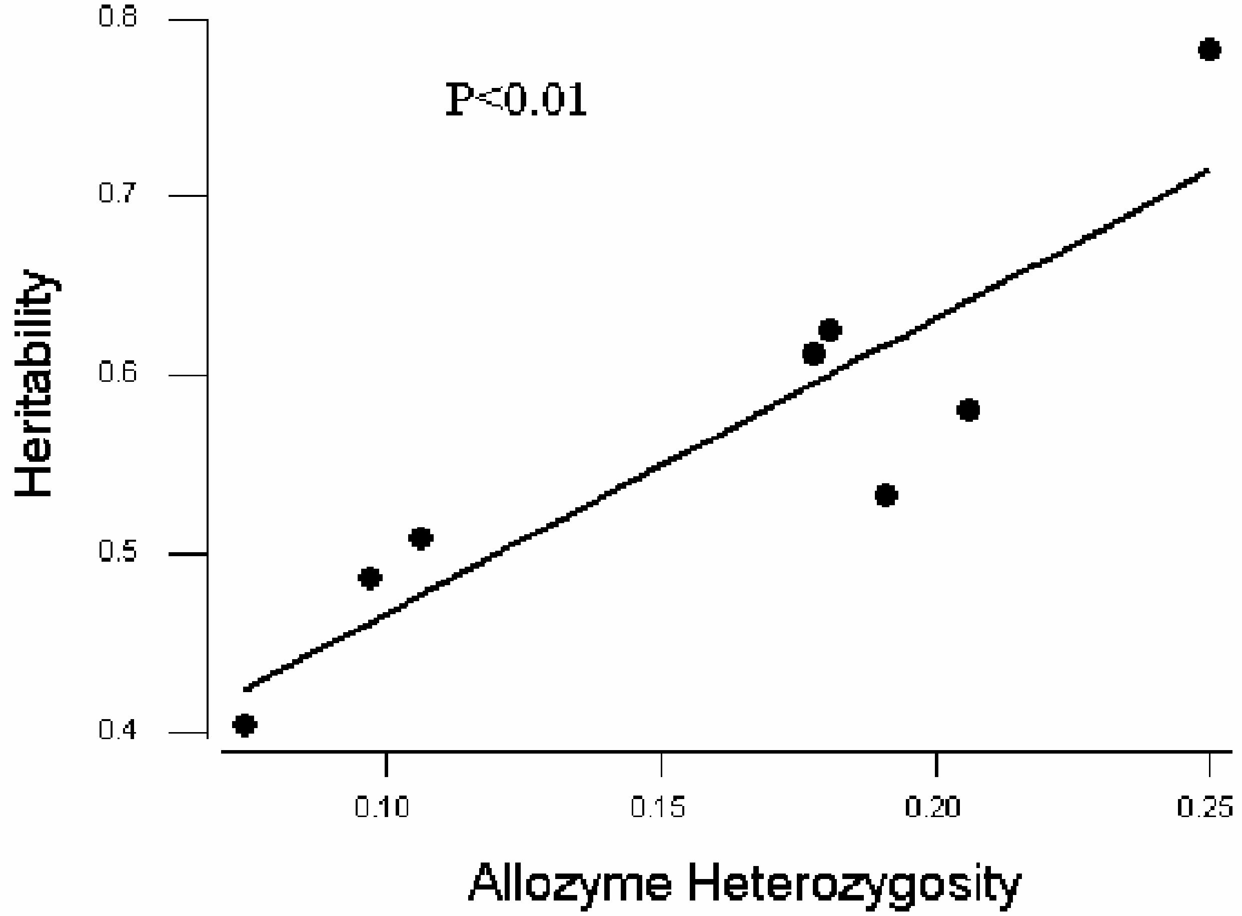


Figure 11.11. Relationship between quantitative genetic variation (H_N for sternopleural bristle number) and molecular genetic variation (heterozygosity at nine allozyme loci) in eight laboratory strains of Drosophila. (from Briscoe et al. 1992)